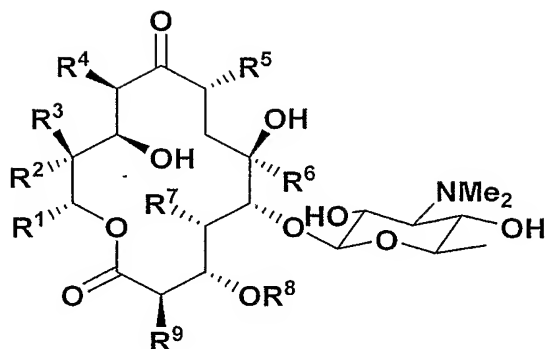
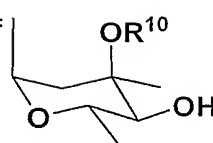


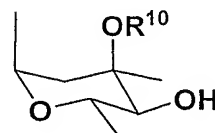
1/23

Figure 1A

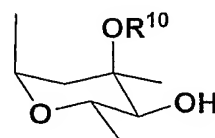
5-O-dedesosaminy-5-O-mycaminosyl-erythromycin B

 $R^1 = C_2H_5 \quad R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3 \quad R^3 = -H \quad R^8 =$


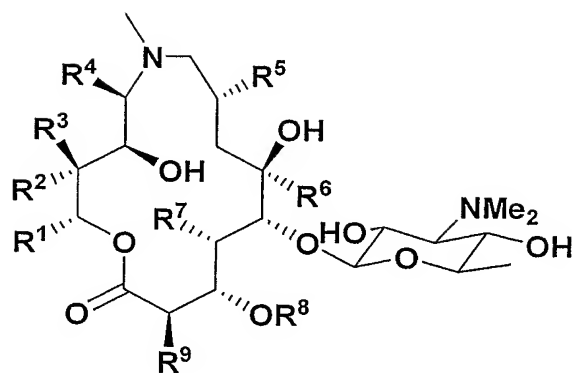
5-O-dedesosaminy-5-O-mycaminosyl-erythromycin A

 $R^1 = C_2H_5 \quad R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3 \quad R^3 = -OH \quad R^8 =$
 $R^{10} = CH_3$ 

5-O-dedesosaminy-5-O-mycaminosyl-erythromycin C

 $R^1 = C_2H_5 \quad R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3 \quad R^3 = -OH \quad R^8 =$
 $R^{10} = H$ 

2/23

Figure 1B

5-O-dedesosaminyl-5-O-mycaminosyl-azithromycin

$R^1 = C_2H_5$ $R^2 = R^4 = R^5 = R^6 = R^7 = R^9 = -CH_3$ $R^3 = -OH$ $R^8 =$
 $R^{10} =$

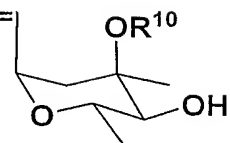


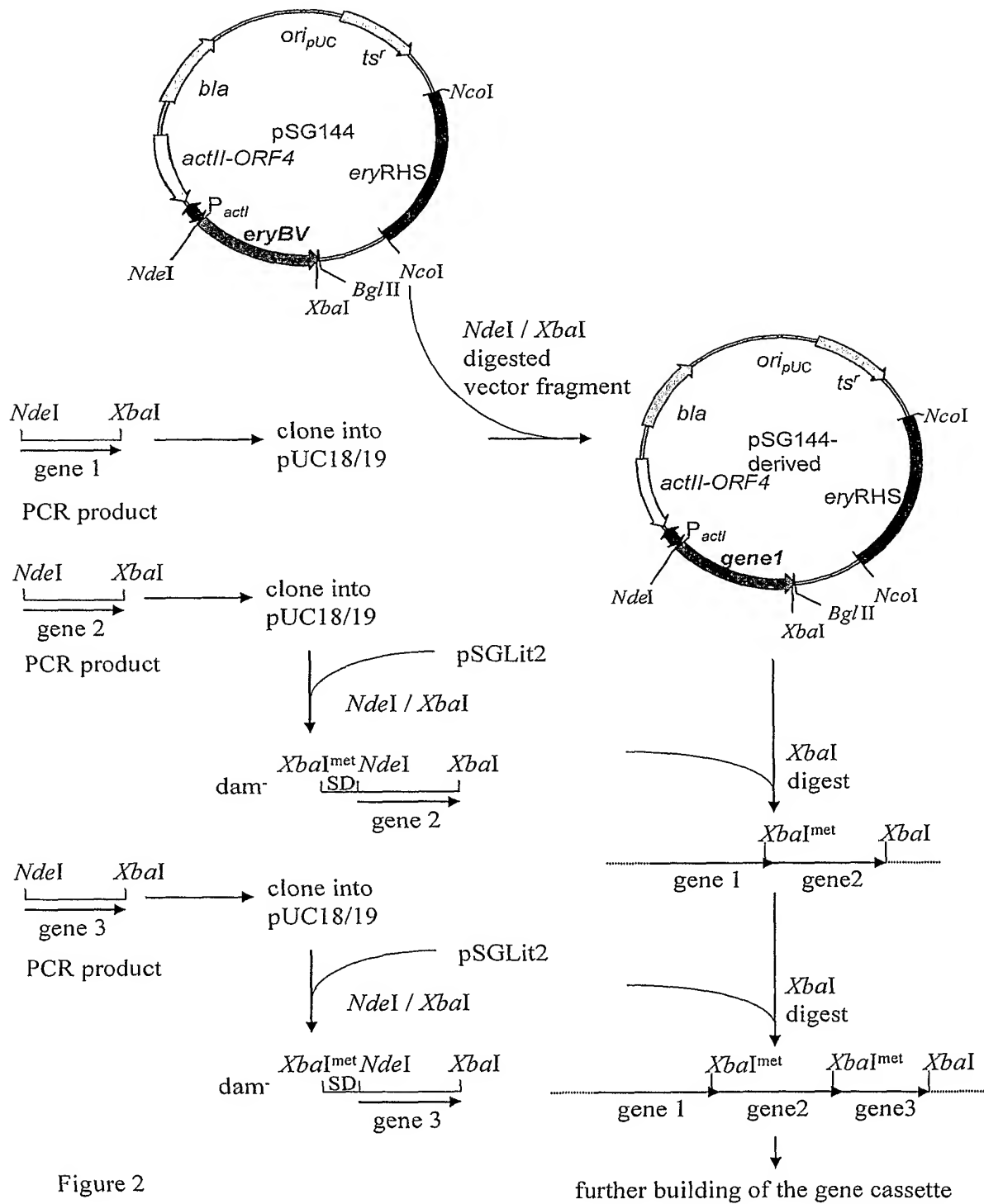
Figure 2

Figure 3

TylA1.pep x u08223.em_pro2

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  |||
10 1 MNDRPRRAMKGIILAGGSGTRLRPLTGTLSKQLLPVYDKPMIYYPLSVLM 50
17 51 LAGIREIQIIS SKDHLDLFRSLLGEGDRLGLSISYAEQREPRGIAEAFLI 100
  |||
17 51 LAGIREIQIIS SKDHLDLFRSLLGEGDRLGLSISYAEQREPRGIAEAFLI 100
24 101 GARHIGGDDAALILGDNV FHGPGFSSVLTGTVARLDGCELF GYPVKDAHR 150
  |||
24 101 GARHIGGDDAALILGDNV FHGPGFSSVLTGTVARLDGCELF GYPVKDAHR 150
31 151 YGVGEIDSGGRLLSLEEKPRRPRSNLAVTGLYLYTNDVVEIARTISPSAR 200
  |||
31 151 YGVGEIDSGGRLLSLEEKPRRPLEP.GRHRLYLYTNDVVEIARTISPSAR 199
38 201 GELEITDVNKNVYLEQGRARLTELGRGFAWLDMGTHDSL LQAGQYVQLLEQ 250
  |||
38 200 GELEITDVNKNVYLEQGRA.AHGAGAVVAWLDMGTHDSL LQAGQYVQLLEQ 248
45 251 RQGERIACIEEIAMRMGFISAEQCYRLGQELRSSSYGSYIIDVAMRGAAA 300
  |||
45 249 RQGERIACIEEIAMRMGFISAEQCYRLGQELRSSSYGSYIIDVAMRGAAA 298
52 301 DSRAQ 305
  |||
52 299 DSRAQ 303

```

35

Figure 4

TylAII.pep x u08223.em_pro2

5

1 MRVLVTGGAGFIGSHFTGQLLT GAYPDLGATRTRVVLDKLTYAGNPANLEH 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

0

51 VAGHPDLEFVRGDIADQALVRRLMEGVGLVVHFAAESHVDRSIESSEAFV 100
|||||
51 VAGHPDLEFVRGDIADHGWRRLMEGVGLVVHFAAESHVDRSIESSEAFV 100

5

```

101 RTNVEGTRVLLQAAVDAGVGRFVHISTDEVYGSIAEGSWPEDHPLAPNSP 150
    |||||
101 RTNVEGTRVLLQAAVDAGVGRFVHISTDEVYGSIAEGSWPEDHPVAPNSP 150

```

10

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 |||
 151 YAATKAASDLLALAYHRTYGLDVRVTRCSNNYGPRQYPEKAVPLEFTTNLL 200

15

201 DGLPVPLYGDGGNTREWLHVDHCRGVALVAAGGRPGVIYNIGGGTELTN 250
 |||
 201 DGLPVPLYGDGGNTREWLHVDHCRGVALVGAGGRPGVIYNIGGGTELTN 250

0

251 AELTDRIELCGADRSAVRRVAD RPGHDRRYSVDTTKIREELGYAPRTGI 300
 |||
 251 AELTDRIELCGADRSALRRVAD RPGHDRRYSVDTTKIREELGYAPRTGI 300

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      |||||
301  TEGLAGTVAWYRDNRRAWWEPLKRSPGGRELER 333

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5

6/23

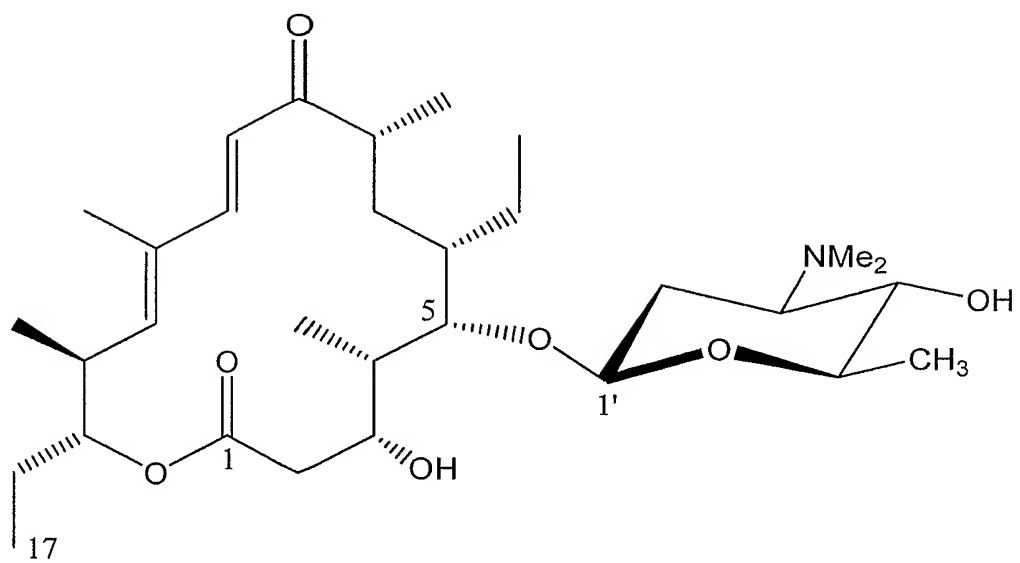
Figure 5

Figure 6

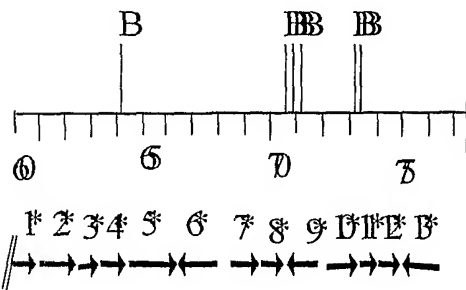
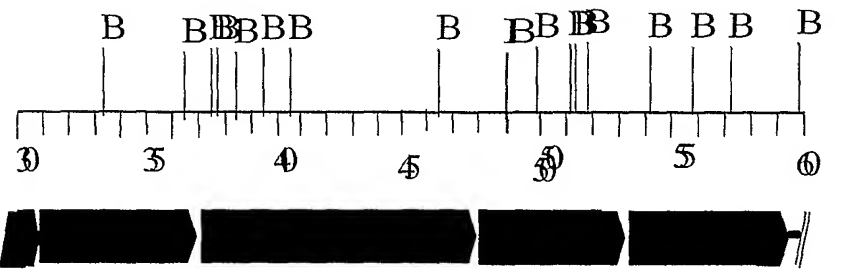
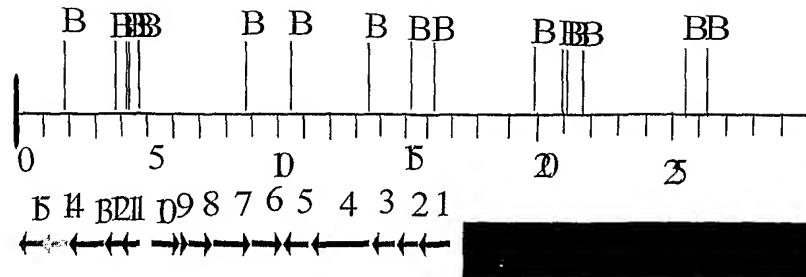


Figure 7

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 51 GTGCAGGGCC GCGATCACCT TGTCTGTAC GTCGGGCGCG AGCCCCGGGT
10 101 ACATCGGCAG CGAGAAGATC TCGTCCGCCA GCCGCTCCGT CACCGGCAGC
 151 GAGCCCTTGG CGTACCCAG GTGCGCGAAG CCCGTCATGG TGTGCACGGG
 201 CCACGGGTAA CTGATGTTGA GCGAGATCCC GTACGACTTG AGCGCCTCGA
15 251 TGATGTCGTC CCGGCGCGGG TGGCGGACGA CGTACACGTA ATACACGTGG
 301 TCGTTGCCCT CGGTGACGGA CGGCAGCACC AGGCCGCCGG GGCCCGTCAG
 351 GTTTCGCGAGT CCTTCGGCGT AACGCCGGGC GACCGCGCGC CGGCCCTCGA
20 401 TGTAGCGGTC GAGGCGGGTG AGCTTGCGGC GCAGGATCTC CGCCTGCACC
 451 TCGTGAGACC GGCTGTTGTG GCCGGGCGTC TGCACGACGT AGTACACGTC
25 501 CTCCATGCCG TAGTAGCGCA GCCGGCGCAG CGCACGGTCG ACGTCCGCGT
 551 CGTCGGTCAG CACGGCCCCG CCGTCGCCGT ACGCACCGAG GACCTTCGTC
 601 GGGTAGAACG AGAAGGCGGC GGCCTCGCCC AGCGTGCCGG CCAGCTCGCC
30 651 GTGGTGGCGG GCACCGTGCG CCTGGGCGCA GTCCTCCAGC ACCACCAGGC
 701 CGTGCTGCTC GGCCAGGGCG CGCAAGGGCG CCATGTCGAC GCACTGCCCCG
35 751 TACAGGTGCA CCGGCAGCAG GGCCTTCGTG CGCGGGGTGA TGACGTCCGC
 801 GACCTGGTCG GTGTCCATGA GGTGGTCCTC GGC GCGGACG TCGACGAAGA
 851 CGGGCGTGGC ACCGGTGCCG TCGATGGCCA CCACCGTCGG CGCGGCCGTG
40 901 TTGGAGACGG TGACGACCTC GTCCCCGGG CCCACCCCGA GCGCCTGCAG
 951 ACCCAGCTTG ACGGCGTTGG TGCCGTTGTC GACACGCCG CAGTGGCGCA
45 1001 GGCCGTGGTA GTCCGGAAC TCCTTCTCGA ACCCGTCCAC GCTGGGGCCG
 1051 AGGACCAACT GCCCGGAGGC GAAGACGGTC TCGACGGCGT CGAGGAGGTC
 1101 CGCGCGTTCG TTCTGGTATT CCGCCAGGTA GTCCCAGACG TAGGTAGTCA
50 1151 CGGAGAGCTC AACCTCCAGA GTGTTTCGAT GGGGTGGTGG GAAGCCGGTG
 1201 CGCGCGGACC AGGTCGTGCC AGCAGTCGCG GACCGACTCC CGCAGCGAAC
55 1251 GGCGCGGTGC CCAGCCCAGC AGGGCGCGCG CCGCGCCGGT GTCGACCCGC
 1301 AGCCAGTCCT CCCGGTGCCC GGGAGCCCGG CCCGGAGCCG GCGCTCCAC
 1351 CACCCGCGCC GGAATGCCGC TCGCTCGAT GAACAGGCCG ACCAGGTCGC
60 1401 GGACGGCGAC CGCCTCGCCC CGCCCGATGC CGACGGCGAC CGGGACGGCC

9/23

5 1451 GGTGCGCGGG CGGCGGCCAC GACGGCGTCG GCCACGTCCC GCACATCGAC
1501 GTAGTCCCGG TGC GCGCGCA GCCGGGACAG TTCCACGACG GCCTCCGCAC
1551 CCGTCCCGGC GGCCGCCAGC AGCCGCTCGG CGACCTGGCC CAGCAGACTG
10 1601 ATCCGCGGGG TGCCGGGGCC CGACACGTTG GACACCCGTA GCACCACACC
1651 GTCGACCCAC CCGCCCGAGG TGCCCCGCAG CACCGCCTCG CTGGCGGCGA
1701 GCTTGCTCCT GCCGTACGCC GTGTCCGGGC GCGGTACGGC GTCGGCGCCC
15 1751 ACCGAACCGC CGGGCGTCAC CGGGCCGTAC TCCAGTACCG AGCCGAGGTG
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1951 GGCGGCCAGC GCCGCGGGAT CCGTACCGGC CAGGTCCAGG GTGACGCAGC
25 2001 GGTACGGCAT CGGCTCCTCG GGCGGGCGGC GGCCACAC CACCACGTCA
2051 CGGCCCCGCG CGGCGAACGC CGCGCACACA TGCCGGCCGA CGTACCCGGC
2101 GCCGCCAGG ACCACGACGC TGCCACTGCC ACTGCCGCGC GGCATCGGAT
30 2151 CGTTCACCAT

10/23

Figure 8

5	11301	CGTCAGTACA	GCGTGTGGGC	ACACGCCACC	AGGGTGCGCA	GCTCGATGTT
	11351	GAGGTAGTTG	CCGTGCGCCA	GCAGCCCGGT	GAGCTGACCG	AGCGACAGCC
	11401	AGGCGAAGTC	GTCCGGTGCG	TCCTCCGGGA	AGTCGTGCGG	GACCTCCACG
10	11451	ATCACGTAGC	GGTTCTGGGC	GTGGAAGAAG	CGCCCGCCCT	CCTCGGACTG
	11501	GACGGCGTCG	TAGCGCACGT	CCTGAGGCGG	CGCGGACAGC	ACGTCCTCCA
15	11551	GGTACGGCGG	GCCGGGCAGC	CCCCGCGGAC	CGGTGTGCTC	CTGTGGCCGG
	11601	CACTGGACCG	TGGGGGCCAG	CTCGGCGACG	TTCAGGTGCC	CGACGTCCAC
	11651	CCGTGCCCCG	ACGAGCGCGT	GCAGCACGCC	GTCGACGGAC	TTGACCAGCA
20	11701	GCGCCATCAG	ACCCGGCAGC	CGCGGCTCGA	TGAGCGGCTG	CGTCCAGGAG
	11751	GTGACCTCCC	GGCTGCTGGC	GCTGACCTCG	GCGGCCATGA	CCCGGAAGTG
25	11801	CCGCCCCGCTC	TCGTGGGCGA	TCTCGTGCGG	CGTGCGGTAC	CAGCCGTCCG
	11851	CCGTCACCGT	ATCGAGCGGC	ACCCGGTTCT	GCACCAGCTC	CCGCAGGGCG
	11901	CGCACACCCG	TGAACCACGT	CAGGACCTCG	GCCGTCTGTGT	GCCGCGCCGC
30	11951	ACCCGGCGAG	CCGAAGAAGG	AGCGCAGCAC	GGGGGACGGG	GCGGACGCGT
	12001	CGGCGTCCGC	CGTGGGCAGG	CAGGCGAGGA	TGGACCGGGC	GTCCATGTTG
35	12051	ACCACGTTGT	CCAGCATCAG	CAGCCGGCGG	AGCTGCCCCA	GCGTCAGCCA
	12101	GCGGAAGTCC	TCCCCGATGT	CGAGGTCGTC	GTCCGCCGCC	AACTCGACGA
	12151	TCATGTTCCG	GTTGCGTTTG	GCCAGGACC	AGTCCGCCTG	TT'CGGACTGG
40	12201	ATCGAGTCGA	CCAGGACACG	CGCCCGTCGC	GGCCCCATGA	ACAGGTCCAG
	12251	ATAGCGGATG	TCGCGCCCCC	GGTGACCCCC	GGTGAAGTTG	CTCCGGGTGG
45	12301	CCTGCACGGT	CGGCGACACC	TGAAGAACGT	TGACGTTCCC	GGGCTCCATC
	12351	TTGGCCTGCA	TCAGGAAGTG	CAGCACCCCG	TCGATCTCCC	GCGCCACGAT
	12401	CCCGAGCAGC	CCCACCTCCG	GCTGCACGAT	GATGGGCTGC	GTCCAGCCCC
50	12451	GCTCGGGCAG	CCGGTCCGTA	CGGACGTGCA	GCCCCCTCCAC	GGAGAAGAAA
	12501	CGGCCCCGACG	CGTGGTGCAG	GTTTCCCGTA	CCCGGGTGGA	AGCTCCAGCC
55	12551	GCGCAGCTCC	GCGAAGGGAA	CGCGGGACAC	GTCGAAGCGC	CCCGCCCCGA
	12601	GGCGTTCCGG	CAGCCAGCCG	GAGATGCCGT	CGAACGGCGT	GACCGCACTG
	12651	TCCGCGGTGC	GTGCCGACAC	CAGCACCCGC	CGCGCCGTGT	CCACCGGGTC
50	12701	ACCGGGCCCG	ACCGCGTCCG	CACGGCGCCG	CGCGGCGCCG	TGCGGGGCGG

11/23

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12801 GGC GGGACGG GGCCGGTGCT CGTGTCCGCG GCGGTACGCG GTGGGACGGT
12851 CCCGGTGGCC GTGTCCGCGG TGGCCGTGCC GGCAGGGGCG TCGCCGATGG
10 12901 TCCGGCACAC CTCGTCCATC CGGTGCTTCA GATAGAAGTG ACCGCCGGCG
12951 AAGGTGTGCA GGGCGAAGGG GCCCGTGGTC AGCTCCCGCC AGGCCCTCGC
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45 13801 GCGGCCTTCT TCAGCGGTTT CCACCACGCG CGGTTCTCCG CGTACCAGCG
13851 CACCGTGTCC GCCAGGCCCG TCGTGAAGTC CGTACGCGGG GCATAGCCCA
13901 GCTCGCCCGT GATCTTGCCG ATGTCCAGCG CGTACCGCAG GTCGTGCCCC
50 13951 GGCCGGTCCG CGACGTGGCG CACCGACGAG GCGTCGGCAC CGCACAGCCC
14001 GAGCAGCCGC TTCGTCAGCT CCCGGTTGGT CAGCTCCGTC CCGCCACCGA
55 14051 TGTGGTAGAC CTCGCCCCGG CGCCCGCGGG TCGCCACCAG GCTGATCCCG
14101 CGGCAGTGGT CGTCCACGTG CAGCCAGTCC CGGCTGTTGC CGCCGTCGCT
14151 GTACAGCGGC ACCGTCAGAC CGTCCAACAG GTTCGTGGCG AAGAGCGGGA
60 14201 CGACCTTCTC GGGGTGCTGG TACGGGCCGT AGTTGTTGGA GCACCGGGTG

12/23

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5 14351 CCTCGCGCCA CGACCCCTCG GCGATCGAGC CGTACACCTC GTCCGTGGAG
14401 ACGTGGACGA ACCGGCCGGC CCCC GCCTCC ACCGCGGCCT GCAAGAGGAC
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10 14501 AGCGGTCCAC GTGCGACTCC GCCGCGAAGT GGACCACGAC GTCCGCCCCC
14551 CGCACGACCC GGGACATCAC CTCCGCGTCC CGGATGTCGG CGTGCACGAA
15 14601 CTCCAGCGAC GGATGGTCCG CGACCGGGTC CAGGTTGGCG AGGTTCCCGG
14651 CATAGGTCAG CTTGTTCGACC ACCACCGTCC GCGCCCCGCG CAGGTCCGGA
14701 TACGCCCCGG CCAGCAGTTG TCTGACGAAG TGCGAGCCGA TGAAGCCCCG
20 14751 ACCTCCGGTG ACCAGCAGCC GCATGGGAGC ACAGACCTTT CTTCCAGGGA
14801 CGGGAAACGG GGAGGCGGAC GGGGACGGAG GCGAGGGCGG TGGCTATGCG
25 14851 GCCGGTCCGG ACATGAGGGT CTCCGCCACG TCCATCAAGT ACCGGCCGTA
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14951 TGTACCCCAT CCGCAGGGCG ATCTCCTCGA CGCAGGAGAT CCGCACGCCC
30 15001 TGCCGCTGCT CCAGGAGCTG GACGTACTGC CCCGCTTGCA GCAGCGAGCT
15051 GTGCGTGCCC ATGTCCAGCC AGGCGAACCC GCGCCCCAGT TCCGTCATAC
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15151 TCGCCCCGCG GCGACGGTGT CAGCCGCCGG GCGATGTCCA CCACGCCGTT
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45 15351 CAGCCGCGCC GCGGTGGAGG CCAGCACGGA GGAGAACCCC GGACCGTGGA
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15451 TCGCCGATGA GGAACGCCTC GGCGATGCCC CGGGGCTCCT CCTGCTCGGC
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15551 ACATCTCCAA GTGCGTCTTC GACGTGATGA TCTGGATGTC CCGGATCCCC
55 15601 GCCAGCATGA GCACCGACAG CGGGTAGTAG ATCATGGGCT TGTCGTAGAC
15651 CGGCAGCAAC TGCTTGGACA GTGCCCCGGT CAGGGGGCGC AGGCGCGTGC
15701 CGCTGCCGCC CGCCAGGATG ATGCCCTTCA TGGGCCGCCG GTCCGCCGTC
60 15751 GTCTTCGTCA T

Figure 9

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	59801	TGAGCCCCGC	ACCCGCCACC	GAGGACCCGG	CCGCCGCCGG	GCGCCGCCTG
	59851	CAACTGACCC	GCGCAGCCCA	GTGGTTTCGCG	GGAACCCAGG	ACGACCCGTA
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	59951	GGATCCGGGC	CCACGGGCCG	CTCTTCCGCA	GCGACCTGCT	CGACACCTGG
15	60001	GTCACGGCGA	GCAGGGCCGT	CGCCGACGAA	GTGATCACCT	CACCCGCCTT
	60051	CGACGGGCTC	ACGGCCGACG	GGCGGCGCCC	CGGCGCGCGG	GAAGTGCCGC
	60101	TGTCCGGCAC	CGCGCTCGAC	GCGGACCGCG	CCACATGCGC	ACGGTTCGGG
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	60451	GCGGAAGCCG	CGCTGACCGC	CGTGCTGGCC	TCCGCCCTGC	GCGGGACTCC
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	60551	CGGCCGCCGA	GCCCCGAGCC	ACCCTCGTCG	GCAACGCCGT	ACAGGAGCTG
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40	60651	GGCCGCCGCG	GTGACCGAAA	CGTGCGTGT	CGCCCCGCC	GTCCGCCTGG
	60701	AGCGGCGGGT	CGCCCGCGAG	GACACGGACA	TCGCCGGGCA	GCGCCTCCCC
45	60751	GCCGGGGGGA	GCGTCGTGAT	CCTCGTCGCC	GCCGTCAACC	GCGCGCCCGT
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	61051	CGCCGCTCAC	CGGTGCTGCA	CGGACACGCC	CGCCTCCCCG	TCGCCGTGCG
	61101	CCGGACGGCC	CGTGACCTGC	CCGCCACCGC	ACCGCGGAAC	TGAGGAGGGA
60	61151	GTGCCCCGAT	GCGTATCCTG	CTGACGTCGT	TCGCGCACAA	CACGCACTAC

14/23

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60 62651 CCGGGGTGGA GATGTCCCC GACATGCTGG CCATCGCGCA GCGGCGCAAC

15/23

62701 CCGGAGGCCG GCATCCACCG GGGGGACATG CGGGACTTCG CCCTCGGCCG
62751 CCGCTTCGAC GCCGTGATCT GCATGTTTCTG TTCCATCGGG CACATGCGCG
5 62801 ACCAGCGGGA ACTGGACGCG GCGATCGGCC GTTTCGCCGC GCACCTGCCG
62851 TCCGGCGGGG TCGTGATCGT CGATCCCTGG TGGTCCCCGG AGACGTTTCTG
10 62901 ACCGGGGTAC GTCGGCGCGA GCCTCGTCTG GCGCGAGGGC CGCACCATCG
62951 CGCGCTTCTC CCACTCCGCG CTCGAGGACG GCGCGACCCG GATCGATGTG
63001 GACTACCTCG TCGGCGTGCC GGGGGAGGGG GTGCGGCACT TGAAGGAGAC
15 63051 CCATCGGATC ACGCTTTTCTG GCGGTGCGCA GTACGAGGCG GCCTTCACCG
63101 CGGCGGGGAT GTCCGTCGAG TACCTCCCGC ACGCCGCCAC CGACCGCGGA
20 63151 CTCTTCGTCG GCGTCCAGGC CTGA

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16/23

Figure 10

1 MKGIILAGGS GTRLRPLTGA LSKQLLPVYD KPMIYYPLSV LMLAGIRDIQ
51 IITSKTHLEM FRSL LGDGSR IGISVGYAEQ EEPRGIAEAF LIGEEHIGDD
101 PVALILGDNV FHGPGFSSVL ASTAARLDGC ELFGYPVKDP RRYGVGEVDA
151 EGRLVSLEEK PEKPRSHLAV TGLYFYDNGV VDIARRLTPS PRGELEITDV
201 NKVYLEQGRA RMTELGRGFA WLDMGTHSSL LQAGQYVQLL EQRQGVRI SC
251 VEEIALRMGY ISARQCHEL G RELESSSYGR YLMDVAETLM SG PAA

Figure 11

1 MRLLVTTGGAG FIGSHFVRQL LAGAYPDLAG ARTVVVDKLT YAGNLANLDP
51 VADHPSLEFV HADIRDAEVM SRVVRGADV VHFHAAESHVD RSIADASAFV
101 ETNVRGTQVL LQAAVEAGAG RFVHVSTDEV YGSIAEGSWR EEQPLAPNSP
151 YAASKAASDL LALAYHRTYG LPVVVTRCSN NYGPYQHPEK VVPLFATNLL
201 DGLTVPLYSD GGNSRDWLHV DDHCRGISLV ATRGRPGEVY HIGGGTELTN
251 RELTKRLLGL CGADASSVRH VADRPBGHDLR YALDIGKITG ELGYAPRTDF
301 TTGLADTVRW YAENRAWWEP LKKAQEARR TD

18/23

Figure 12

5
1 VSTPSAPPVP GAPSPAGHPD EGLWVRRYRP VRDPELRLVC FPHAGGAATS
51 FAALARGLDE TVEALAVQYP GRQDRRHEFF IPSISGLVDQ VVPEILRWAD
101 RPLALFGHSM GATVAFEVAR RLRGSGQASP VHLLVSGRRA PTVRRRDVAH
10 151 LLDDDALIAE IATLQGTEDA VLQDEELLRL ALPAIRNDYR AAGTYAYVPG
201 GALDCPVTVL TGDRDPDVPL EEARAWRELT TGPFALHTFA GGHFYLNDRM
251 DEVCRTIGDA LAGTATADTA TGTVPPTAA DTSTGPVPPR TAADTAREPV
15 301 PPRSAPAPHG AARRRADAVR PGDPVDTARR VLVSARTADS AVTPFDGISG
351 WLAERLRAGR FDVSRVPFAE LRGWSFHPGT GNLHHASGRF FSVEGLHVRT
20 401 DRLPERGWTQ PIIVQPEVGL LGIVAREIDG VLHFLMQAKM EPGNVNVLQV
451 SPTVQATRSN FTGVHRGRDI RYLDLFMGPR RARVLVDSIQ SEQADWFLAK
501 RNRNMIVELA ADDDLDIGED FRWLTGQLR RLLMLDNVNN MDARSILACL
25 551 PTADADASAP SPVLSFFGS PGAARHTTAE VLTWFTGVRA LRELQNRVP
601 LDTVTDGWY RTPHEIAHES GRHFRVMAAE VSASSREVTS WTQPLIEPRL
30 651 PGLMALLVKS VDGVLHALVR ARVDVGHLNV AELAPTVQCR PQEHTGPRGL
701 PGPPYLEDVL SAPPQDVRYD AVQSEEGGRF FHAQNRYVIV EVPHDFPEDA
751 PDDFAWLSLG QLTGLLAHGN YLNIELRTLIV ACAHTLY
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19/23

Figure 13

5 1 MVNDPMFRGS GSGSVVVLGG AGYVGRHVCA AFAARGRDVV VVGRRPPEEP
 51 MPYRCVTLDL AGTDPAALAA ALDAERPDTI VNSVGSIWGR TDEQMWSATA
 101 VPTLRLLEAL ALMSARFRLV HLGSVLEYGP VTPGGSVGAD AVPRPDYAYG
0 151 RSKLAASEAV LRGTSGGWVD GVVLRVSNVS GPGTPRISLL GQVAERLLAA
 201 AGTGAEAVVE LSRLRAHRDY VDVRDVADAV VAAARAPAVP VAVGIGRGEA
5 251 VAVRDLVGLF IEASGIPARV VERPAPGRAP GHREDWLRVD TGAARALLGW
 301 APRRSLRESV RDCWHDLVRA HRLPTTPSKH SGG

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Figure 14

5 1 VTTYVWDYLA EYQNERADLL DAVETVFASG QLVLGPSVDG FEKEFADYHG
 51 LRHCGGVDNG TNAVKLGLQA LGVGPGEDEVV TVSNTAAPT VVAIDGTGATP
10 101 VFVDVRAEDH LMDTDQVADV ITPRTKALLP VHLYGQCVD M APLRALAEQH
 151 GLVVLEDCAQ AHGARHHGEL AGTLGDAAAF SFYPTKVLGA YGDGGAVLTD
 201 DADVDRALRR LRYYG MEDVY YVVQTPGHNS RLDEVQAEIL RRKLTRLDRY
15 251 IEGRRAVARR YAEGLANLTG PGGLVLPSVT EGNDHVYYVY VVRHPRRDDI
 301 IEALKSYGIS LNISYPWPVH TMTGFAHLGY AKGSLPVTER LADEIFSLPM
 351 YPGLAPDVQD KVIAALHEVL ATL
20

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Figure 15

5 1 VSPAPATEDP AAAGRRLQLT RAAQWFAGTQ DDPYALVLRA EATDPAPYEE
 51 RIRAHGPLFR SDLLDTWVTA SRAVADEVIT SPAFDGLTAD GRRPGARELP
10 101 LSGTALDADR ATCARFGALT AWGGPLLAP HERALRESAE RRAHTLLDGA
 151 EAALAADGTV DLVDAYARRL PALVLREQLG VP EEAATAFE DALAGCRRTL
 201 DGALCPQLLP DAVAGVRAEA ALTAVLASAL RGTPAGRAPD AVAAARTLAV
15 251 AAAEPAATLV GNAVQELLAR PAQWAEIVRD PRLAAAVTE TLRVAPPVRL
 301 ERRVARETD IAGQRLPAGG SVVILVAVN RAPVSAGSDA STTVPHAGGR
 351 PRTSAPSVPS APFDLTRPVA APGPFGPLPGD LHFRLGGPLV GTVAEALGA
20 401 LAARLPGLRA AGPAVRRRRS PVLHG HARLP VAVARTARDL PATAPRN

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22/23

Figure 16

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1 MRILLTSFAH NTHYYNLVPL GWALRAAGHD VRVASQPSLT GTITGSGSLTA
51 VPVGDDTAIV ELITEIGDDL VLYQQGMDFV DTRDEPLSWE HALGQQTIMS
101 AMCFSPNLGD STIDDMVALA RSWKPDVLVW EPFTYAGPVA AHACGAAHAR
10 151 LLWGPDVVLN ARRQFTRLLA ERPVEQREDP VGEWLTWTLE RHGLAADADT
201 IEELFAGQWT IDPSAGSLRL PVDGEVVPMP FVPYNGASVV PAWLSEPPAR
15 251 PRVCVTLGVS TRETYGTDGV PFHELLAGLA DVDAEIVATL DAGQLPDAAG
301 LPGNVRVVDF VPLDALLPSC AAIVHHGGAG TCFTATVHGV PQIVVASLWD
351 APLKAHQLAE AGAGIALDPG ELGVDTLRGA VVRVLESREM AVAARRLADE
20 401 MLAAPTPAAL VPRLERLTAA HRRA

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Figure 17

5 1 MNLEYSGDIA RLYDLVHQK GKDYRAEAE LAALVTQRRP GARSLLDVAC
 51 GTGMHLRHLG DLFEEVAGVE MSPDMLAIAQ RRNPEAGIHR GDMRDFALGR
10 101 RFDVICMFS SIGHMRDQRE LDAAIGRFAA HLPSSGGVVIV DPWWFPETFT
 151 PGYVGASLVE AEGRTIARFS HSALEDGATR IDVDYLVGVP GEGVRHLKET
 201 HRITLFGRAQ YEAAFTAAGM SVEYLPHAAT DRGLFVGVA

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